

Page 1 of 19 TREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

P65#26 -> Genes DNA sequence 1665 b.p. gaattcggcttc ... caagccgaattc linear

602 196 752 246 302 96 452 146 527 171 152 46 377 121 677 221 227 71 CTG 9 0 0 929 CAG GAC GCA A GAC AAA GCT AAC N 7 F T AAA ATC GCT **GGT** 66T 6 66T 6 GTA. V <u>9</u>10 CAG **GGT** 299 ATG ၅၁၁ GCA AAA AAC ACC CGT CGC R AAA GCA AAAAAAGAC D AGC A A GAA E 66T 6 CTG CTG ATG 929 GAT D ACC 101 GAA E GAA ATG M CTG AAG GAC GCG A **TT**G GTA GAT 611 AA A ATG GTG GAA 22GAA E GAC D ACC GCT 6T6 V GTT V ဗ္ဗ GAC D GTA GAA GTA V GAA E **GGT** Jec GCT A CGT R CTG GAC AAC <u>გეე</u> გეე ATC CTG GCA AAC N GCT A ATG CTG GAA GTA 399 GAA E CGT. **GGT** GAC D 5 ATC 299 221Α¥ GAC D ACT ဥ္သမ္မ AAC N CIGK AA GAA E 939 CTG CAG 0 GAA 66T 6 GCT 66T 6 CCA P GTA V CTG , 500 900 900 GAC GCA GCT CGT TTC F AAG ე<u>ფ</u> AAC AAA GCA ACC T **GGT** GTT A A A CTG CTC GTA 939 ၁၁၅ GAA E ACC AAC N ၁ဗ္ဗာ GTA V AAA AAA GAA ATC ACC GAC D 202 6 6 GAC D CTG AAC GAC GAA TCT TCC S GTT V GTT Α¥ ΑA ၁၁၅ 299 AAC N GAA TAC GTT **GGT** GCT A GTG V GAA CCT GAT D GCT GTT GCT GCG A AAA GAA ACC T GCA A X A A ACT GCT 700 101 gaattcggcttcat ATG M CTG AAG AAA ATC ACT ATC GAT D GCT GCA A ATC **GT**G ATC GTC **6TG** TAC ATG CTG CC 299 299 ACC GCT 66T 6 GTA: V CAG CAG CTG ეე გე AAA K GAA CGT GTT 78 22 228 378 122 528 172 678 222 303 453 147 603 197 53 97

FIG. 14

Page 2 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

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1052 346 1502 496 1202 396 1652 546 1665 1352 446 1127 371 1427 471 127. 421 1577 521 GTG V TGA * GTA V X A A A GCA A CGC GCC A GTT V GT / ATG M GCG A ATC I CGC R CGC R CGC R $^{\mathsf{A}}$ ATT I CTG L GTG V ATG M GTA V GCC A CTG 76C GGT 66T 6 X A A GCG A GCG A ACC GAG E 66A S S S CGC R GAG E AAG K ე<u>9</u>9 AAC N GTT V GTT V CAG Q GAG E ATG M ATG M A A A ACC 9 GCT A CTG L AAA K ATC GTG V GAC D ATC I 9 9 AAC GGT G ATG M GTA V ATC I ATG M ე<u>ე</u>9 GAA E A A GGT G 66T 6 GTA V GAA E GAC D gAA E GCT A S AAC 9 5 6 ၁၉၅ GTT V GTT V CGT R . 199 . 199 AAA 676 V GAC D GAA E GTG V CAG Q GAG E 9 6CG A AAA ACT 66T 6 GAA E GAC D GAA E ၁၅၅ 9 TAC Y TAT Y ACT T GCT A cg R GT) GCG A GAA E 9 9 GAC D GAA E GAA E TCT S GCT A GAG GAA AAC 76C C GAA E GCG A 700 S GCT A GCT A 66T 6 GTA V CAG 0 AAC N ATG M E.AA ACT T GGT G ACT T CTG L 6CG A GCA A ၁၅၅ ACC T GCA A TAC GAC GTT V 66T 6 . 199 GTA V GAA E AAA K A A A CAG 0 ATC I ACC GAA E GCT A GCT A CCT GAG E GAA E ATC I ATC I AAC N CGT R CAA O GAA ACC TAC Y GAT D ე ე GAT GTT V GA D GAA E A A CAG GCG A GCC A GCT A ე<u>ე</u> CGT R 66T 6 TCT S S CAG 0 TAC Y AAA K CAC H ATT GTT V . R C ე<u>ფ</u> CTG L A A A 500 P AAC N GTA V CTG L ე<u>ე</u>9 GCC A TCC S TCT S 66T 6 ATT I GCA A CAG Q 606 A GAA E AAA K GAC D GAT D GAC D 5 [5 × CTG L GTA V ATG M GAA E ACC T ACC T S R G G 66T 6 ACT T 66.T 6 1578 522 1278 422 1353 447 1428 472 753 247 978 322 1128 1203 397 503 497 1053 347

FIG. 1B



Page 3 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

P65#44 -> Genes DNA sequence 1654 b.p. gaattcggcttc ... aaagccgaattc linear use to subclone for expression

452 146 602 196 7.52 246 152 46 302 96 527 171 677 221 227 71 377 121 ည AAA SA ACA T ACA T **GGT** <u>61</u>T GGT ATC I S ည္ဟ CAA GAC D. CGT GAT D 9 GCT **GGT** 999 ე<u>წ</u> CGT ATT S S CAG TAC AAT AAT CGT GCT GTT CGT AGC AAG K GAA gcA GAA A A CGT GTC. V GAA E AAA CAA GAA GGA AAT ATG M ACA ATG GAA GAA **GGT** AAT CAT LI GCT GAC ATC ည္ဟ **GCA** GTA GTT V ACT CTT S **GGA** CCA AGC S GTC V <u>611</u> GAA E GAC CGT R GAA AAT N GAT AAT TCT S GCT GCC A **6TG** က် က ATC GAA ĀTC **GGT** E GAT D ATG GCA OTC GAG 66T 6 TAC ATT **GGT** S AAA X A A A GAA E GCA AAC GAG E ACA TCA S CCA P GAA AAA AAC GAA GAT **GGT** AAA 66A 6 ATG ည္ဟ GIC AAT GTT AGC S X A A A 116 TTG ACC AAC AAA GAT D GAA ATT **66T** ATT I AAA AAA GAA ACA T CAA ACT GCT ACT T CGT GAA E GTA V GTGTCA 676GAA TCA TCT A A A GAG ATG. X A A A GGA CCT **CGT** AAT 66T 6 GCA A 5 GTA GAA GAA 00GAC D TAC ſCT GTT V ATG M GAA CAG 0 gcA AAT CGT TCT ACT gaattcggcttcat ACC GAT D TCA ည္ဟ **GTA** TCA GTA AAG ATT <u>E</u> 11G TTG GÁC D GCA **GCA** GTC GCA TAC CIT 153 47 228 72 378 122 528 172 603 197 678 222 78 303 97 453 147



Page 4 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

1502 496 1202 396 1052 346 1127 371 1352 446 1427 471 1654 542 1277 421 1577 521 977 321 827 271 676 V GAA E 66A 6 6T6 V TCA S GAT D ATI 5 ccaaagccgaattc GAA E 6T6 V GAA E **GAG** AAC N AAT N GCC AAT N ATT I GCT 6TT ' E > GTA V GCC A GCC A CGC R AAT N GCT A . . TGA * A A GTC V CAC CTC GAT D . . . A A GCA A 66A 6 CGC GCT A 66T 6 ATG M ACA T ATC GAA E ე<u>ფ</u> GAA E 6TT V CGT R E H I ACA T GCG A S S GAA E 66A 6 GAT D 66T G GCT A ATC I CAA 66A 6 GAA E TT6 L $^{\mathsf{AAA}}$ AAC N 66T 6 AAT N TTG L AA A 66T 6 CCT P CGT R GAT D 66T 6 GTT V ATG M ACA T GAG E GCA A ATC I GAA E 66A 6 ATT I AAT N E > ATG M ATG M GCG A 66A 6 ACA T GTT V ACT T TCT S CGT R GCA A 66A 6 AGT S GCA A GAC GAA E ATT AAC N AGC S GAA. E GAA E GCC A A A P CA SGC R 66T 6 ACT T 66T 6 E L 2 GTA V GAA E GAA. E GCA A GAA E 766 W GAT D GAT D CGT GAG E GCC A GAA E 66A 6 66A 6 GAG E TCT S. GCT A TCT S GCA A 66A 6 ACA T GCA A 9 9 6 GCA A GTT V ACT T GTC V GCA A ACA T AAT N GCT A 66T ဥ္ပြင္ ACG T AAG K GCA A GAA E CAC GCA A AAT N GAT D ACT T E 116 GCA A CAA Q AGC S GAA E GAC D ATT I GCT A CGT R CTA L GCC A ATC I GTT V ACC T E GA GAT D ACT T GTA V GCG A GCC A ACA T $^{\mathsf{A}}$ CAA 0 GCT A GAT D GCT A GTA V TCA S AAC 66A 6 GCG A GTC V ATC GAC D CGT R TCT S GTT V AAG K CTC ATA I GAA E 66T 6 200 GTT V GC. GT) GT > GTA V ACA T ATC I GCC A CCA P 66T 6 CCA P ACC T CCT P AGT S 66T 6 1578 522 1128 372 1278 422 1353 447 1503 497 753 247 978 322 1053 347 1203 397 903 297

FIG. 2B



Page 5 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

Y65#5 -> Genes DNA sequence 1662 b.p. gaattcggcttc ... caagccgaattc linear

452 146 602 196 752 246 677 221 302 96 152 46 377 121 527 171 227 71 77 CAG CTG 933 d 606 A GAC A A A GAC GCT AAC N ATC AAA 299 GCT 66T 9 9 9 GTA V 299 **GGT** ე<u>ფ</u> AAA ACC CGT AAA AAA AGC AAA A A K GAA GAT D **GGT** 909 CTG ATG GAA. E GAA GAC D 101 6CG A CIG CTG L AAG GAC GAT D A A A 6TGGAG GTG V GAC D ATG TCT GAA E GTA V CCA **16**C 909 GAA GTA V GAC GAA GGT CGT R CTG 900 600 ATC I AAC N GAC AAC N GCT GCT A ATG M GTA CTG L GAA E 299 CGT R GĀĞ E ဥဗ္ဗ GAC D 399 201 AAA K GAC D ACT 299 AAC N ط GAA CTG GAA E 929 A A GAA **GGT** 66T 6 ATG GTA CTG CCA 909 900 b CGT R GAC GCT AAG ე<u>წ</u> AAC GIT AAA ACC 66T 6 A A A CTGGAA AAC CTG ၁၁ဗ ACC GTA V AAA GAA ATC GAC D AA **GGT** ACC GAT D CTG GAC AAC GTA V GAA GTT V AA A GAA TAC 22 ၁၁ဗ AAC A A **GGT** GGT **GT** GCT A GTG GAA GAT D GTT V <u>E</u> 606 A AAA 221 GAA TCC GCA A ACC AAA K ATG M AAG CTG GAC D ACG AAA ATC ATC gaattcggcttcat GTG 676GAC ATC GTC ACC T GCA A LAC GCT AT6 ၁၅ **66T** CTG 66T 6 GCT GCT CTG CAG GAA CAG 0 A A GTA V ၁ဗ္ဗာ GTA CCA P 528 172 78 153 47 228 72 303 378 122 453 147 603 197

FIG. 3A



Page 6 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

1052 346 1202 396 1352 446 1427 471 1653 545 1502 496 1577 521 127. 421 977 321 827 271 tcaa GCA A GCA A GTG V X A ACC T CGT R GT / TGA * 6T6 V A A CGC R CGC R ATC I 2 R GTG V ATG M CTG L CTG L 29 29 20 GCA A ၁၉၆ ၁၅၅ GAG E 6CG A 6CG A A'AC N ¥¥ S R G G CGT R GTG V AAC ACC T A A GGT G 66T 6 CAG Q ACC GCG A GAG E A A A 66T 6 GTG V A A ATC I 908 A AAC 66T 6 ATG M GAA AA K 66T 6 66T 6 GTT ATG M GAA E GTG V CTG L GAA E GTG V GAC D GCT A TCT 66T 6 AAC N GTT V AAC CTG L 9 CGT R 6TT V CAG GAG E GTG V ე<u>ი</u> ლ 6T6 V GAC GAA E ACC ည္တတ TAC 9 GAA E TAC GTC V GCA A GAA E 9 6 6 GAT D 6CG A CGT R ACT GCG A GAA E GAA E GAA E TCT S CGC R GAT D GAT D GGT G GCT A GAA E GAA E AAC N 66T 6 6CG A GCT A GTA V CAG 0 AAC N GAA ATC I 66T 6 GTC V 6CG A TCC GCA A TAC Y GCC A GCT A ၁ဗ္ဗဗ GTG V GCA A CAG Q ACC GAA E A A A CCT E GA 299 GCT A ACT T CTG L GCA A ATC I AAC N ACC T CGT R GTA V ACC 990 9 TAC v GAC D GCG A 0 0 0 X A CAG GCG A TCC S RGT R 66T 6 \sum_{i} CTG CTG L TAC Y AAA K AAG K CAC H AAC GTT V CGT R CTĞ L AAA K AAC N ACC T CCT CGT R 66T 6 CTG L 9 9 GCC A GCG A 66T 6 5 > GAA E GAC CAG 0 GCC GAA E GCA A GAT D GTT V ATG M CTG L GAC D 9 6 6 ACC T GTT V 986 GGT G . . 1578 522 1278 422 1353 447 1203 397 903 297 753 247

FIG. 3B

1654

Page 7 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001



Y65#21 -> Genes DNA sequence 1661 b.p. gaattcggcttc ... TAAgccgaattc linear V261 - same in clone Y65#24, too used to subclone for expression !!!

ATG M GAT D GTT V GGA G CGC R GTG V ATG M GCC A GCT CGT R 909 A Y60-2 GAT D GCA A S A A A ATC T GAA E A A GCA A ATG M gaattcggcttcat

302 96 452 146 602 196 152 46 377 121 677 221 527 171 227 71 ည AAACAA ACA T GTC ACG 66T 6 66T 6 GCA CAG 0 GAT CGT TCI AAC GGT 999 ၁၅၅ 616 AAC CGA CAA 55 AAA GAA GCA GAA E CGT CGT R AAG K GAG 299 GAA AAC GAA ATG GAA ე<u>ე</u> ე **GGT** ACG GCT **GTT** TCT GAT <u>61</u>1 GTA GAA GTG GAC 999 CCA GAA GTT S GAA GCA AATAAT GAT GAA ATC S S S CT **GGT** GCT Ē GAA ATG 999 TAT <u>66</u>1 5 GAG AAA AAA GAG GAA GAA GAT GCC A **GGA** AAA CCT P AAT GTG AAA66T 6 GCT GTT ACC AAA CT AAT **GGT** GAA ACG AAA AAA CGA ACC ၁၁၅ GTA V CTA GTA GAA E GTC TCT TCT 999 GAA AAA 66A 6 ၁ဗ္ဗာ SCT GTT **GTG** GAA E TCA GAA TAC GTC V GAC GCT CAA ACA TCA ACC AAT GAA CAT H GCA GTA ACT ACC TCT GAT D TCT **GTT** GCA **GTG** ACA T GCA GTG TAC TTA TTA TTG GCC A GCA GCT 228 72 378 122 453 147 528 172 603 197 22 153 303

FIG. 4A

752 246

CIC

AAC

ACC

GAA

GAG

CTA

CCA

CAA

ATC

AAC

TCA

6TG

AAA

AAA

GAT D

Page 8 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

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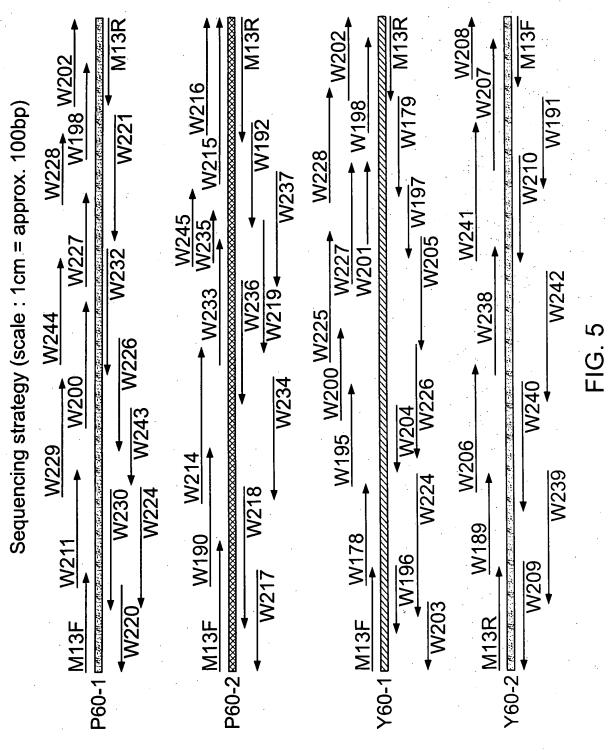
1052 346 1202 396 1352 446 1127 371 1502 496 1652 546 1427 471 1577 521 127. 421 977 321 827 271 TAA A 6TG V CTG L GAG E GTA V 6 6 GAT D ATT I AAG K GAG E GAA E GTT V . 199 ACG T CTA X A GTC V AGC 9 9 GCG A ATG M SGC R AAC N ACT T CGT R ATT I GCT A CCT P ∐ > AAC N GAC D CGT R GGT E3 GCA A A A CTT CGT R 2 2 GTG V AAG GA. ACA T ATC GAA E GAC D CAA O GAA 66A 6 GAC D 66A 6 ACA T GCT ATT I CTA L ACA T AAC N GAA E AAA K AAC. N 66A G GGT G A A X A 66T 6 CGT R GTC V 66A 6 GCT A ATT AGT S ACA T ATG M ATG M 66A 6 GTT V ACT T CGT R GAG E ATC I ACC S GAC D 9 GAT D GCT A GAT D GAA E CCA P 66T 6 66T 6 GAT D GTT V ТGG w GAA E GAC CCA P GAA E TAC CTT GAT D GCA A GAA E 999 6 GAG E TCT S 9 9 6 GCT A GTI E GAA GAG E 66A G ACT T GTT V GCT A GCT A H က္တ GTA V GTA V ACA T GCC A ACA T AAT N 66T 6 ACA ΑA GCA A GAG E GGA G GAT D GTG V AGC S GAA GAT CGT R CT 5 SC. 606 A GAG E ACA T GAT D GCT A AATGAT D E > A A A A GCT A GCT A GAT D GCT A GCA A TCG S GTA V GTA V 66A 6 CCA P GAT D AAT N CGT R CTA L GTG V GTA V ACA T $^{\mathsf{A}}$ AAA K GAA E 66T 6 GT1 V ATI I 66A 6 ACA T GAA E ACA T ATT I GTT V ATT I GGT GCT A CCT P CCT 753 247 1053 347 1128 372 1203 397 1278 422 1353 1503 497 1578 522

FIG. 4

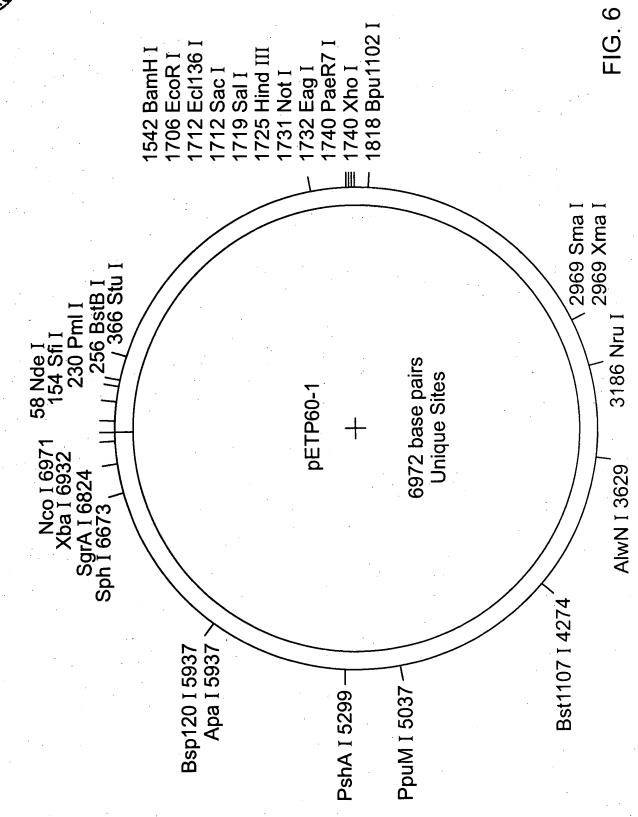
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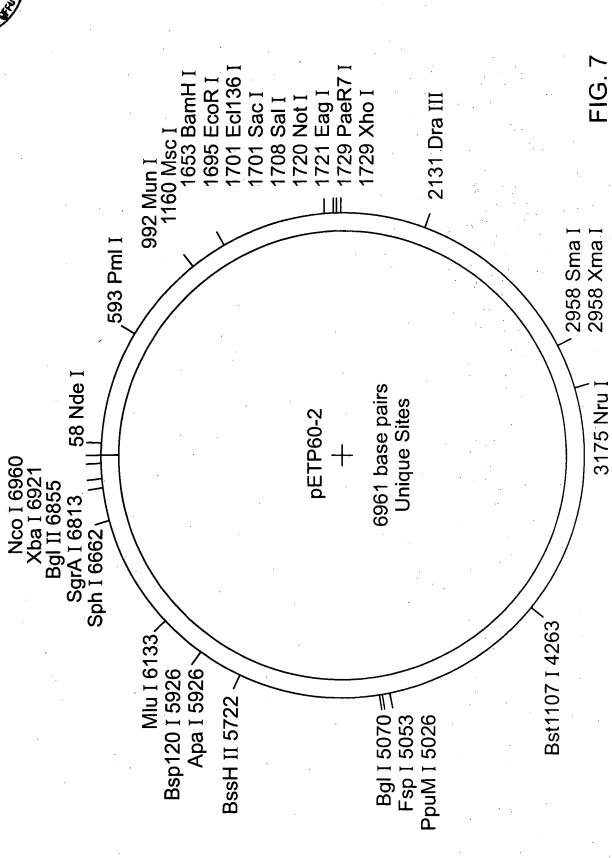




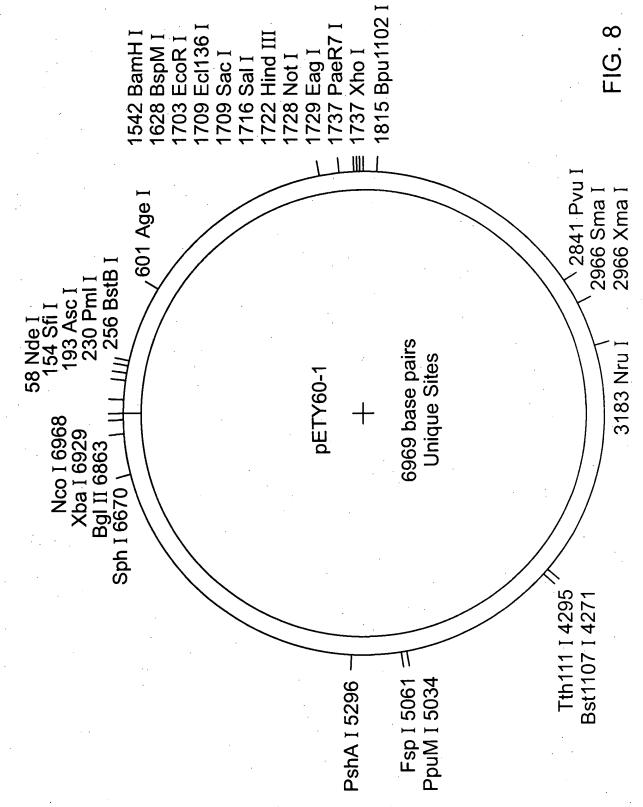


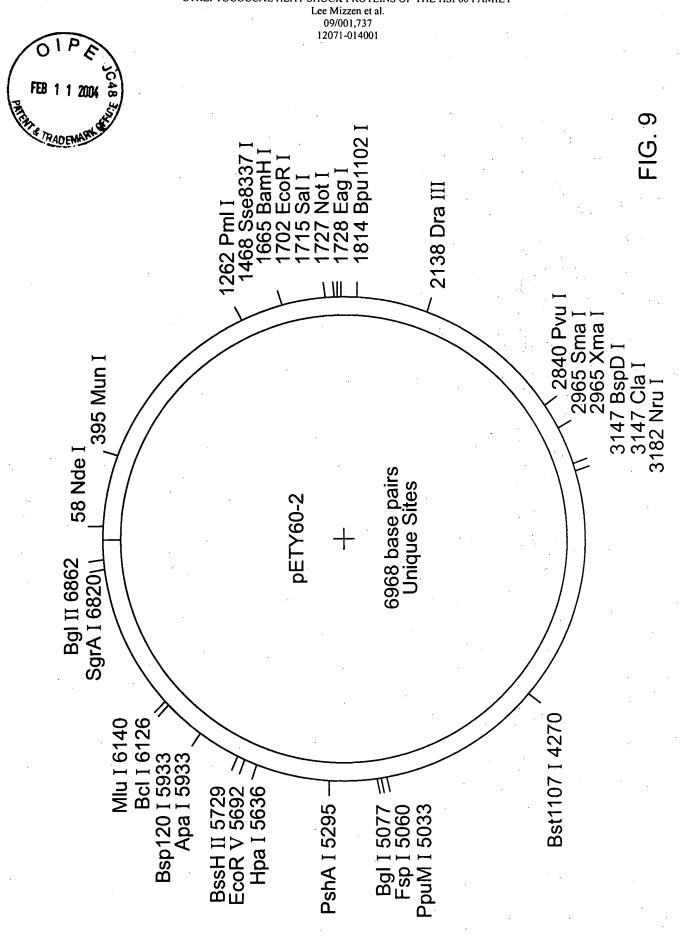














Page 14 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

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KDIKFGEEARRAMLRGVNALADAVKVTLGPKGRNVVLEKSFGAPTITKDGVTVAKEIELEDKFENMGAQLVKEVASKTNDV 	AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVARETELEDKFENMGAQMVKEVASKANDA AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVARETELEDKFENMGADMVKEVASKANDA	KEIKFSSDARSAMVRGVDILADTVKVTLGPKGRNVVLEKSFGSPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDI	KEIKFSADARAAMYRGVDMLADTVKVTLGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDI KEIKESERABAMI BENDAAMIAAAVIVII CDKCANIVII EKKECSRIITANGVTIAKEIELEDA ERIMGAVIIA GIASKITINDI	-KIINTSEEAKRAMEKAVIDALADAKVANTKIERKANIVYLENKIASTLIIMOSYIIAKEIELEDATENMOANLVAEVASKIINOV -KTILEGEEARRSMOAGVOKLANTVKVTLGPKGRNVILDKKEGSPLIINOGVTIAREIELEDAVENMGAOIVKEVATKINOV	-VVTGEQLDKSIREVVRILEDAVGCTAGPKGLTVAISKPYGAPEVTKDGYKVMKSIKPEDPLALAIANIIAQSASQCNDK	AKDVKFGNDARVKMLNGVNILADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAREIELEDKFENMGAQMVKEVASKANDA	NELKTBUDAKLYMLAGVNALADAVŲV IMGENGKNAV VELKAJIGAPI VI NOGVAVANELIETENTMINIGAĻMV NEVARKTODU KTTAVDEFARRGI FRGI NAI ADAVKVTI GPKGRNVVI FKKWGAPTITNDGVSIAKFIFI EDPYFKIGAFI VKFVAKKTODU	EEAF	KLIEYDETARHAMEVGMNKLADTVRVTLGPRGRHVVLAKAFGGPTITNDGVTVAREIDLEDPFENLGAQLVKSVATKTNDV	KTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAELVKEVAKKTDDV	KLI EYDETARRAMEVGMDKLADTVRVTLGPRGRHVVLAKAFGGPTVTNDGVTVAREI ELEDPFEDLGAQLVKSVATKTNDV	KDVQFGNEVRQKMVNGVNI LANAVRVTLGPKGRNVVDDRAFGGPHI TKDGVTVAKE I ELKDK FENMGAQMVKEVASKTNDV	KQLKFSEDARQAMLRGVDQLANAVKVTIGPKGRNVVLDKEFTAPLITNDGVTIAKEIELEDPYENMGAKLVQEVANKTNEI	KSLIYNDEARRALERGMDILAEAVAVTLGPKGRNVVLEKKFGSPQIINDGITIAKEIELEDHVENTGVSLIRQAASKTNDV	KLISFKDESRRSLEAGINALADAVRITLGPKGRNVLLEKQYGAPQIVNDGITVAKEIELSNPEENAGAKLIQEVASKTKE	-KTIAFDKKARRGLERGLNALADAVKVTLGPKGRNVVLEKKWGAPTITNDGVSTAKEIELEDPYEKIGAELVKEVAKKIDDV KRIKESKRARASSI I TRYRET ABANSVI SPREGRANI I PRABESSERVITKARSKISI KRKESII SABINONIKASKISIK	¥ 2 3	-SSHKELKFGVEGKASLLKGVETLAEAVAATLGFKGRNVLTEQFFGFFTTTNGGVTVAKSTVLADNFERMGANLLGEVASNTNEA -SKDTPFGSDARTAMTTGCNKTADAVSVTTGPKGRNVTTFOSFGSPKTTKDGVTVAKSTFFNNKLANTGAOMVKOVAANTNGK	-VYSGEOLOGAFREVAAVIDSTVAVTAGPRGKTVGINKPYGAPEITKDGYKVMKGIKPEKPLNAAITŠIFAQSCSQCNDK	A EGF	PEV	ADA!	EA.	OHS!
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FIG. 10A

	76	SPYFI	SQYMV	SQYMV	SPYMV	SAYMV	SPYFI	SPYFY	SGYFV	SGYFV	SAYFV	SGYFV	SAYFV	SPYFI	SPYMV	SPYFV	SPYFI	SGYFA	SPYFI	SPYFI	SPYFI	SPYFI	SPYFI	SPYFI	SPILL	SPYFI	SPOFV	
	1 250	EDGTGLQDELDVVEG-MQFDRGYLSPYF EDGTGI FDFI DVVFG-MOFDRGYI SPYF	QFDRGYL	EESRGMETELEVVEG-MQFDRGYLSQYM	EESKGFTTELEVVEG-MQFDRGYASPYM	EESKSMGTELDVVEG-MQFDRGYVSAYMV	EDGTGI EDEI DVVEG-MOFDRGYI SPYF	EDGNGLENELS VVEG - MOFDRGY I SPYFY	EESNTFGLQLELTEG-MRFDKGYISGYF\	EESNTFGLQLELTEG-MRFDKGYISGYF	ESSTLDTELEFTEG-VGFDKGFLSAYF\	EESNTFGLQLELTEG-MRFDKGYISGYF	EESSTLGTELEFTEG-IGFDKGFLSAYF	EDGKSLENELDVVEG-MQFDRGYLSPYF;	EESNRLNTELELG-MQFDRGYQSPYM	EEGKSMTTELEITEG-MRFDKGYISPYF	EESKSLNTELEVVEG-MQIDRGYISPYF)	EESNTFGLQLELTEG-MRFDKGF1SGYF/	KEGRTISDELEVTEG-MKFDRGYISPYF	REGRTLEDELEVTEG-MRFDRGFISPYF)	FEGKTLQHELEIVEG-IKFDRGYISPYF	-IADAVKKVGKEGVITVEESKGSKELEVELTTG-MQFDRGYLSPYF	KDGKTLNDQLELIEG-MKFDRGYISPYF	KOGKTLTDELEVIEGTMRFDRGYISPYF KOCKTINDELETIEG MKEDBCVISBNET	NOGNI LINDELETTEG-MAT DAGITSFT	ADGNTLYNELEVYEG-MKLDRGYISPYI	ESSNSFETTVEVEEG-MEIDRGYISPQF	
		-EDGTGLQDELDVVEG-MQFDRGYI -EDGTGLFDFIDVVFG-MOFDRGYI	EESRGMETELEVVEG-MOFDRGYI	EVVEG-M	EVVEG-M	DVVEG-M	DVVF6-M	SVVEG-M	ELTEG-M	ELTEG-M	EFTEG-V	ELTEG-M	EFTEG-I	DVVEG-M	ELG-M	EITEG-M	EVVEG-M	ELTEG-M	EVTEG-M	EVTEG-M	EIVEG-I	ELTTG-M	ELIEG-M	EVIEGTM	FVVFCLN	EVVEG-M	EVEEG-M	
	 240	TGLQDEL TGL FDF1	RGMETEL	RGMETEL	KGFTTEL	KSMGTEL	TGI EDFI	NGLENEL	NTFGLOL	NTFGLQL	STLOTEL	NTFGLOL	STLGTEL	KSLENEL	NRLNTEL	KSMTTEL	KSLNTEL	NTFGLQL	RTISDEL	RTLEDEL	KTLOHEL	KELEV	KTLNDQL	KTLTDEL	KTI FNFI	NTLYNEL	NSFETTV	
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	190	SDSKAIA SDSKAIA	ANKEAIA	SGKEAIA	EGKESIA	NGKEDIARVAAISA-ADEKIGK	ETSKEIE	KDSKAIA	ETKDQIA	ETKEQIA	AGKDAIT	ETKEQIA	SGKTGIA	DTSKEIA	ENKNEIA	GDSKAIA	-EGSAIA	ETKDQIA	TTSEEIS	TTSEEIA	TTEEIF	EKIDEVA	TTPEEIA	STPEEIA	CTOFFIA	STSFFIA	KGGDDIK	
	180	LSVPC	NVIPV	IAQPV	ISKPI	ISKPV	AGMNPMDI KRGTOKAVNSVVAFI KNI SKPC	MSKTC	SAKEV	GAKEV	.VATPV	DAKEV	SATPV	IAKPC	NSQKV	HA0PV	VAKPV	AAKEV	NKRDI	NKKEI	IKKDV	MARTISL	ISKKV	MSRPV	LADMI	MARMI	LARPV	
	-	AVEELKA AVEELKA	AVEALKN	AVEALKA	AIENLKE	AVEEI QK	VVAFIKN	VTKKLQA	VTETLLK	VTETLLK	VSEALLA	VTETLLK	VSEALLA	LVEELKN	AVEALHE	LVARIKE	LVQEIEA	VTEHLLK	VVEFLQA	VIEFLSA	VLEYLNS	VLKEVAS	VVAELKK	VKDNLKT	VIAELEN	VVTNIKE	LVEELEK	
	170	AGMNPMDLKRGIDKAVAAAVEELKALSVPC AGMNPMDLKRGIDKAVASAVEELKALSVPC	AGANPIGIRRGIETAVAAAVEALKNNVIPV	AGANPIGIRRGIETATATAVEALKAIAQPV	AGANPVGVRKGMEQAVAVAIENLKEISKPI-	AGANPILIRNGIKTAVEKAVEEIQKISKPV	TOKAVIS	AGMNPMDLKRGIDKAVLAVTKKLQAMSKTC	AGANPLGLKRGI EKAVEKVTETLLKSAKEV	AGANPLGLKRGI EKAVEKVTETLLKGAKEV	AGANPVALGAGISKAADAVSEALLAVATPV	AGANPLGLKRGI EKAVDKVTETLLKDAKEV	AGVNPIALGVGIGKAADAVSEALLASATPV	AGMNPTDLKRGIDKAVAALVEELKNIAKPC	SGANPVGLRQGIDKAVKVAVEALHENSQKV	AGANPISLKRGIDKATDFLVARIKEHAQPV-	AGANPVALRRGI EKVTT FLVQEI EAVAKPV	AGANPLGLKRGI EKAVEAVTEHLLKAAKEV	AGCNPMDLRRGIQLAVDNVVEFLQANKRDI	AGCNPMDLRRGSQVAVEKVI EFLSANKKEI	SGMNPMDLLRGINKGVEKVLEYLNSIKKDV-	AGNDRISIKNGMQKAKDVVLKEVASMARTISI	SRGNAVEIRRGVMNAVEVVVAELKKISKKV	KGGNPVEIRRGVMLAVETVKDNLKTMSRPV	KGANPVEIKKGVMLAVDAVIAELKKQSKPV ACMNAMDI PPGISMAVDAVVINI KSKAPMI	AGMNAMDI RRGI SMAVDAVVINI KGMARMI	SGANPVSIKKGIDKTVAALVEELEKLARPV	
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	150	IITEGLK IITEGLK	IVREGIK	IVHEGLK	MIREGLK	IIREGLK VIEEVSK	TVNFGLK	1LVEGHK	LVREGLR	LVREGLR	LVKGGLR	LVKEGLR	LIKGGLR	IVAEGMK	MIQEGLK	IVKEGLR	LVREGLR	LVREGLR	IFSETVR	IFTESVK	I FQQGCK	MIVEASK	IAKEGFE	IAKEGFE	IAKEGFE	1 FT FGCK	IIKLGLL	
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		S.pneumoniae S.pvogenes hs	S. pneumoniae	S. pyogenes hs	B.subtilis gr	Clostridium h	Haemophilus	L. pneumophila	M.avium hsp60	M.bovis hsp60	M. leprae groE	M.lepra	M.tuberculosi	N.meningitidi	S.aureus hsp6	Synechocystis	Synechocystis	Tsukamurella	S.pombe hsp60	S.cerevisiae	P. falciparum	Onchocerca hs	C.elegans hsp	D.melanogaste	numan nspou	maize hsn60	RUBISCO chape	

AGDGTTTATVLAQAIVKEGLKNVAAGANPMDLRRGIDKAVDAVVEELKAIAKPV--ETKEEIAQVATISANGDEEIGE---LIAEAMEKVGKEGVITV---EEGKTLETELEVVEG-MQFDRGYISPYFI



Fage 16 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

329 356 357 331 390 NKPETGAVELESPFILLADKKISNIREMLPVLEAVA--KAGKPLLIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLED-LGQAKRVVINKDTTT DSEKWVADLENPYILITDKKISNIQEILPLLESIL--QSNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILIGGTVITED-LGLELKDATIEA-LGQAARVTVDKDSTV TDNEKMVADLENPILITDKKVSNIQDILPLLEEVL--KTNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITED-LGLELKDATMTA-LGQAAKITVDKDSTV TDPKSSKVEFEKPLLLLSEKKISSIQDILPAL-EISNQS-RRPLLIIAEDVDGEALAACILNKLRGQVKVCAVKAPGFGDNRKNTIGDIAVLTGGTVFTEE-LDLKPEQCTIEN-LGSCDSITVTKEDTV NTSKGQKCEFQDAVVLLSEKKISSIQSIVPAL-E1ANAH-RKPLVIIAEDVDGEALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHD-LGKVGEVIVTKDDAM TNQKTQKCELDDPL1L1HEKKISSINSIVKVL-ELALKR-QRPLL1VSEDVESDALATL1LNKLRAGIKVCA1KAPGFGENRKANLQDLAÅLTGGEVITDE-LGMNLEKVDLSM-LGTCKKVTVSKDDTV INSKAQKCEPEDPLILIHDRKVTNMHAVVKVL-EMALKK-QRPLIVAEDVESEALGTLIINKLRAGIKVCAVKAPGFGENRKANLQDLAILTGGEVITEE-LGMNLENVEPHM-LGSCKKVTVSKDDTV INPEKSIVEFENARVLITDGKISAIKDIJPLLEKTT--QLRAPLLIISEDITGEALATLVVNKLRGILNVAAIKAPGFGERRKALLQDIAILTGAEFQASD-LGLLVENTTIEQ-LGLARKVTISKDSTT DSDKMEAVLDNPYILITDKKITNIQEILPVLEQVV--QQGKPLLLIAEDVEGEALATLVVNKLRGTFNAVAVKAPGFGDRRKAMLEDIAVLTGGEVITED-LGLDLKSTQIAQ-LGRASKVVVTKENTT TDFDNQQAVLEDALILLHQDKISSLPDLLPLLEKVA--GTGKPLLIVAEDVEGEALATLVVNAIRKTLKAVAVKGPYFGDRRKAFLEDLAVVTGGQVVNPD-AGMVLREVGLEV-LGSARRVVSKDDTV TDAERQEAVLEDPYVLLVSGKISTVKDLLPLLEKVI--QSGKPLAIIAEDVEGEALVTLIVNKIRGTFKSVAIKAPGFGDRRKAMLQDMAILTGGQVISEE-IGLSLDTAGLEV-LGQARQVVVTKDETT TNNEKMIVELDDPYLLITEKKLNIIQPLLSILEAVV--KSGKPLLIIAEDIEGEALSTLVINKLRGGLKVAAVKAPGFGDRRKEMLEDIAALTNAKYVIKDELGIKMEDLTLED-LGJAKNVKITKDNTT NSSKGAKVEFQDALLLLSEKKISSVAEHHSPLWRLASRRTRKPLVITAEDIDGEALSTLVVNRLKIGLQVAAVKAPGFGDNRKSTLTDMA-TSGGIVFGDDVSLVKLEDVKVSD-LGQVGEVVITKDDTL TNSEKMLVEFENPY1LLTEKKLNIIQPLLPILENIA--RSGRPLLIIAEDVEGEALSTLVLNKLRGGLHVAAVKAPGFGDRRKDMLGDIAILTGAKHVINDELAIKMEDLTLCD-LGTAKNIRITKDTTT NKPETATVELDNPFILLVDKKISNIRELLPVLEGVA--KAGKPLLIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIAILTAGTVISEE-IGMELEKATLED-LGGAKRIVINKDNTT TDAERMEAVLEDPRILITDKKINLVQDLVPILEQVA--RQGKPLLITAEDIEKEALATLVVNRLRGVLNVAAVKAPGFGDRRKQMLEDIATLTGGQVISED-AGLKLESATVDS-LGSARRINITKDNTT NN--SQKVELDKPY1L1HEKKISTVKSLLPVLEHV--LQNQSSLLV1AEDVDSDALATLIVNKLRLGLKICAVKAPGFGENRKALIHDIAVMTGAKVITEET-GLKLDDPQVVSYLGKAKSINVTKDSTL TDSEKQKAELEDPLILLTDKKISNIQDLLPVLEEVA--QAGKPLLIIAEDVEGEALATLVVNKLRGTLKVVAVKAPGFGDRRKAMLQDIAILTGGQVISEE-LGLSLEDATLED-LGQAKKVVVTKDDTT NKPETGAVELESPFILLADKKISNIREMLPVLEAVA--KAGKPLVIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLED-LGQAKRVVINKDTTT TDTEKMEAVLDNPLVLITDKKISNIQDLLPLLEQIV--QAGKKLLIIADDIEGEAMTILVVNKLRGTFTCVGVKAPGFGBRRKEMLQDIATLTGGVVISDE-VGGDLKEATLDM-LGEAESVKVTKESTT NNQQNMSCELEHPFILLVDKKVSSIREMLSVLEGVA--KSGRPLLIIAEDVEGEALATLVVNNMRGIVKVCAVKAPGFGDRRKAMLQDIAILTKGQVISEE-IGKSLEGATLED-LGSAKRIVVTKENTT TDAERQEAVLEDPF1LLVSSKVSTVKDLLPLLEKVI--OAGKPLLIIAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLODMAILTGGOVISEE-VGLSLESADISL-LGKARKVVVTKDETT NDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQVA--KASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTVISEE-VGLSLEKATLDD-LGGAKRIEIGKENTT TDSDKMVAELERPYILVTDKKISSFQDILPLLEQVV--QSNRPILIVADEVEGDALTNIVLNRMRGTFTAVAVKAPGFGDRRKAMLEDLAILTGAQVITDD-LGLDLKDASIDM-LGTASKVEVTKDNTT TDSDRQLVEFDNPLILITDKKISAIAELVPVLEAVA--RAGRPLLIIAEDIEGEALATLVVNKARGVLNVAAIKAPAFGDRRKAVLQDIAILTGGSVISED-IGLSLDTVSLDQ-LGGAVKATLEKDNTI TSAKGAKVEYEKALVLLSEKKISQVQDI VPAL-ELANKL-RRPLVI IAEDVDGEALTTLVLNRLKVGLQVVAI KAPGFGDNRKNALKDMGIATGAS I FGDETLDLRLEDI TAND-LGEVDEVTITKDDTL TDFDSQQAVLDDPLVLLHQEKISSLPELLPMLEKVT--ESGKPLLIVAEDLEGEALATLVVNSIRKTLKAVAVKSPFFGDRRKAFLEDLAIVTGGQVVNPE-TGLVLREVGTDV-LGSARRVVVSKDDTI TDVKSQKVEFENPLILLSEKKVSAVQDILPSL-ELAAQQ-RRPLVIIAEDVDGEALAACILNKLRGQLQVVAIKAPGFGDNRRNMLGDLAVLTDSAVFNDE-IDVSIEKAQPHH-LGSCGSVTVTKEDTI TDPERQEAVLEDPYILLVSSKVSTVKDLLPLLEKVI--GAGKPLLI1AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEE-VGLTLENADLSL-LGKARKVVVTKDEI TDAERQEAVLEEPYILLVSSKVSTVKDLLPLLEKVI--QAGKSLLIIAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLTLENTDLSL-LGKARKVVMTKDET 360 8 Haemophilus h M.bovis hsp60 S. pyogenes hs S.pyogenes hs Clostridium h Cowdria hsp60 L.pneumophila M.avium hsp60 M.leprae groE M.leprae hsp6 N.meningitidi S.aureus hsp6 Synechocystis C.elegans hsp O.melanogaste RUBISCO chape B.subtilis gr M.tuberculosi Synechocystis S.pombe hsp60 Onchocerca hs S.pneumoniae S.pneumoniae sukamurella S.cerevisiae P. falciparum human hsp60 Arabidopsis maize hsp60

FIG. 10C



Page 17 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

454 IV-SE-NRVTDRVKARIEQIKSQIESST-SDYDKEKLRERLAKLSGGVAVLKVGGATELEVKERRDRVEDQLHATRAAIEEGIVPGGGVALLYASSALDKLKGA--DDEEQIGINIIKKVLSVPIKRLVK IMKGAGDH--VKVNDRCEQIRGVMADPNLTESEKEKLQERLAKLSGGIAVIKVGASSEVEVNEKKDRIVDALNAVKAAVSEGVLPGAGTSFVKASLRLGDIPTN--NFDQKLGVEIVRKAITRPAQTILE LLKGKGKK--DDVLRRANQIRTKIEDTT-SEYEKEKLQERLARLASGVA-LRVGGSSEVEVNEKKDRVHDALNATRAAVEEGIVPGGGRPLLRCIEKLEGVETT--NEDQKLGVEIVRRALRMPCMTIAK VEGSGS--SEAIANRIALIKSQLETTT-SDFDREKLQERLAKLAGGVAVIKVGAPTETALKEMKLRIEDALNATRAAVEEGIVAGGGTALTTVIEKVAALELE---GDDATGRNIVLRALEEPVROIAL IVEGAGD--TDAIAGRVA0IROEIENSD-SDYDREKLOERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTLLQAAPTLDELKLE---GDEATGANIVKVALEAPLKOIAF VVDGDGD--ENSIDARVSQLKSQIEETE-SDFDREKLQERLAKLAGGVAVIKVGAASETELKERKLRIEDALNSTRAAVEEGIVAGGGTALVNVYQKVSENEAE---GDIETGVNIVLKALTAPVRQIAE LVAGADKRASAGVKERIEQLRKEYAASD-SDYDKEKIQERIAKLAGGVAVIKVGAATETELKDRKLRIEDALNATKAAVEEGIVPGGGTTLIRLAGKIESFKAQLSNDEERVAADIIAKALEAPLHQLAS ILNGSGPK--EAIQERIEQIKGSIDITTINSYEKEKLQERLAKLSGGVAVIRVGGASEVEVGEKKDRYDDALNATRAAVEEGILPGGGTALVKASRVLDEVVVD--NFDQKLGVDIIRKAITRPAKQIIE IMEGEGKK--EEINERCESIRNAIKMNT-SDYEKEKLQERLAKITGGVALIKVGGISEVEVNEIKDRIQDALCATKAAVEEGIVPGGGSALLFASKELDSVQTD--NYDQRVGVNIIKDACKAPIKQIAE LLRGRGDQ--TEIEKRIEEITDEIERST-SDYEKEKLNERLAKLSKGVAVLKIGGGSEVEVGEKKDRVTDALCATRAAVEEGIVPGGGVALLRSLTALKNYKAA--NEDQQIGVNIVKKALTQPIATIVK LLKGKGDK--AQIEKRIQEIIEQLDVTT-SEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPA--NEDQKIGIEIIKRTLKIPAMTIAK : LDGAGDK--KGIEERCEQIRSAIELST-SDYDKEKLQERLAKLSGGVAVLKIGGASEAEVGEKKDRVTDALNATKAAVEEGILPGGGVALLYAARELEKLPTA--NFDQKIGVQIIQNALKTPVYTIAS ILDGAGDK--KSIEERADQIRSAVENST-SDYDKEKLQERLAKLSGGVAVLKIGGASEAEVGEKKDRVTDALNATKAAVEEGIVPGGGVALLYASKELDKLQTA--NFDQKIGVQIIQNALKTPVHTIAS IIDGVGD--EAAIQGRVGQIRKQIEEAT-SDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVDDALHATRAAVEEGVVAGGGVALVRVAAKLSGLTAQ--NEDQNVGIKVALRAMEAPLRQIVS IIDGIGD--EAQIQGRVAQIRQQIEEST-SDYDKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEEGIVAGGGVALIRAAGRVVGLQGE--MEEQNVGIKLALRAMEAPLRQIVA IIDGEGK--ATEINARITQIRAQMEETT-SDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEEGIVAGGGVALIRAQKALDSLKGD--NDDQNMGINILRRAIESPMRQIVT IVEGAGD--TDAIAGRVAQIRTEIENSD-SDYDREKLOERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVPNAKAAVEEGIVAGGGVTLLQAAPALDKLKLT---GDEATGANIVKVALEAPLKOIAF IIDGFGD--AAQIEARVAEIRQQIETAT-SDYDKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALLRARAALENLHTG--NADQDAGVOIVLRAVESPLROIVA IVDGAGS--KEQIAGRVSQIRAEIENSD-SDYDREKLQERLAKLAGGVAVIKAGAATE-DLKERKHRIEDAVRNAKAAVEEGIVAGGGSSLAQSGTVFDSXALE---GDEATGANIVKVALDAPVKQIAV IIADAASK--DELQSRVAQLKKELSETD-SIYDSEKLAERIAKLSGGVAVIKVGAATETELEDRKLRIEDAKNATFAAIEEGIVPGGGTALVHLSGYVPAIKEKLEDADERLGADIVQKALVAPAALIAQ IIDGVGD--EAAIQGRVTQIRQQIEEAT-SDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEEGVVAGGGVALIRVASKIAGLKGQ--NEDQNVGIKVALRAMESPLRQIVL ---GDEATGRNIVLRALEEPVROIAH VEGAGE--TDKISARVTQIRAQVEETT-SEFDREKLQERLAKLAGGVAVIKVGAATETELKERKLRIEDALNSTRAAVEEGIVSGGGTALVNVYNKVAAVEAE---GDAQTGINIVLRALEEPIRQIAH VNGRGN--SEFIKNRINQIKLQLEATT-SEFDKEKLQERLAKLAGGVAVVKVGAATETELKESKLRIEDALAATKAAVEEGIVPGGGTAYVNVINEVAKLTSD--IQDEQVGINIIVRSLEEPMRQIAH I-GSVDNSCAHVQSRICQIRMQIDNST-SDYDKEKLQERLAKLSGGVAVLKVGGSSEVEVKERKDRVEDALHATRAAVEEGVVPGGGAALLYTLSALDNLKSK--NDDEQLGINIVKRALQAPIKRIIK VEGAGD--SDAIAGRVAQIRTEIENSD-SDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVALLHAIPALDELKPE---GEEATGANIVRVALERPLKGIAF !VDGGG--SNDAVAKRVNQLRAE1EVSD-SEWDREKLQERVAKLAGGVAVIKVGAVTETALKKRKESVEDAVAAAKASIEEGIIAGGGSALVQCG-AALKQLRTSLTGDEALGIDVFFEALKAPLYWIAT 'VDGGG--TAEAVANRAKHLRAEIDKSD-SDWDREKLGERLAKLAGGVAVIKVGAATETALKERKESVEDAVAAAKAAVEEGIVPGGGASLIHQARKALTELRASLTGDEVLGVDVFSEALAAPLFWIAA IVAEGNE---AAVKSRCEQIRRQIEETD-SSYDKEKLQERLAKLAGGVAVIKVGAATETEMKDRKLRLEDAINATKAAVEEGIVPGGGTTLAHLAPQLEDWATGNLKDEELTGALIVARALPAPLKRIAE !VDGAGD---AAIAGRVAQIRSQIEEST-SDYDKEKLQERLAKLAGGVAVIKVGAATEVELKERKDRVEDALNATRAAVEEGIVPGGGVALLRAAPALDKLKTE--NGDEATGVNIVLRALEAPLRQIAE :VEGAGN--PEAISHRVAVIKSQIETTT-SEFDREKLQERLAKLSGGVAVIKVGAATETELKEMKLRIEDALNATRAAVEEGLVAGGGTALANVIPAVATLELT 490 88 450 430 420 90 Synechocystis O.melanogaste RUBISCO chape g Cowdria hsp60 L.pneumophila M.leprae hsp6 ynechocystis Onchocerca hs C.elegans-hsp S.pyogenes hs Clostridium h Haemophilus h M.avium hsp60 M.bovis hsp60 M.leprae groE N.meningitidi S.aureus hsp6 S. pombe hsp60 S.pyogenes hs M.tuberculosi sukamurella .ceravisiae S. pneumoniae S. pneumoniae P.falciparum human hsp60 Arabidopsis maize hsp60 B.subtilis

FIG. 10E



Page 18 of 19 STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY Lee Mizzen et al. 09/001,737 12071-014001

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FIG. 10E

